9E5

1638

1600 #3

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/021,657

DATE: 01/15/2002
TIME: 19:02:43

RECEIVED

FEB 0 6 2002

TECH CENTER 1600/2900

Input Set : A:\1148.app
Output Set: N:\CRF3\01152002\J021657.raw

ENTERED

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 3 <110> APPLICANT: ALBERTSEN, MARC C.
 4          FOX, TIM
 5          HUFFMAN, GARY
 6          TRIMNELL, MARY
 8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
 9          METHOD OF USING SAME
11 <130> FILE REFERENCE: 1148
13 <140> CURRENT APPLICATION NUMBER: US/10/021,657
14 <141> CURRENT FILING DATE: 2001-12-14
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1906
22 <212> TYPE: DNA
23 <213> ORGANISM: Zea mays
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26 <221> NAME/KEY: CDS
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31 Glu Phe Gly Thr Arg Glu Ala His Leu Thr Pro Ala Thr Pro Ser Pro
32   1               5                   10                  15
34 ttc ttc cca cta gca ggg cct cac aag tac atc gcg ctc ctt ctg gtt      96
35 Phe Phe Pro Leu Ala Gly Pro His Lys Tyr Ile Ala Leu Leu Leu Val
36                   20                  25                  30
38 gtc ctc tca tgg atc ctg gtc cag agg tgg agc ctg agg aag cag aaa      144
39 Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys
40               35                  40                  45
42 ggc ccg aga tca tgg cca gtc atc ggc gca acg gtg gag cag ctg agg      192
43 Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg
44       50                  55                  60
46 aac tac cac cgg atg cac gac tgg ctt gtc ggg tac ctg tca cgg cac      240
47 Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His
48   65                  70                  75                  80
50 agg aca gtg acc gtc gac atg ccg ttc act tcc tac acc tac atc gct      288
51 Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala
52                   85                  90                  95
54 gac ccg gtg aat gtc gag cat gtc ctc aag act aac ttc acc aat tac      336
55 Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr
56                   100                 105                 110
58 ccc aag gga atc gtg tac aga tcc tac atg gac gtg ctc ctc ggt gac      384
59 Pro Lys Gly Ile Val Tyr Arg Ser Tyr Met Asp Val Leu Leu Gly Asp
60                   115                 120                 125
62 ggc atc ttc aac gcc gac ggc gag ctg tgg agg aag cag agg aag acg      432
63 Gly Ile Phe Asn Ala Asp Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr
64       130                 135                 140
66 gcg agt ttc gag ttc gcc tcc aag aac ctg agg gat ttc agc gcc att      480
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Input Set : A:\1148.app
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 67 Ala Ser Phe Glu Phe Ala Ser Lys Asn Leu Arg Asp Phe Ser Ala Ile
 68 145             150             155             160
 70 gtg ttc aga gag tac tcc ctg aag ctg tcg ggt ata ctg agc cag gca    528
 71 Val Phe Arg Glu Tyr Ser Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala
 72             165             170             175
 74 tcc aag gca ggc aaa gtt gtg gac atg cag gaa ctt tac atg agg atg    576
 75 Ser Lys Ala Gly Lys Val Val Asp Met Gln Glu Leu Tyr Met Arg Met
 76             180             185             190
 78 acg ctg gac tcc atc tgc aag gtt ggg ttc ggg gtc gag atc ggc acg    624
 79 Thr Leu Asp Ser Ile Cys Lys Val Gly Phe Gly Val Glu Ile Gly Thr
 80             195             200             205
 82 ctg tcg cca gat ctc ccc gag aac agc ttc gcg cag gcg ttc gat gcc    672
 83 Leu Ser Pro Asp Leu Pro Glu Asn Ser Phe Ala Gln Ala Phe Asp Ala
 84             210             215             220
 86 gcc aac atc atc atc acg ctg cgg ttc atc gac ccg ctg tgg cgc atc    720
 87 Ala Asn Ile Ile Ile Thr Leu Arg Phe Ile Asp Pro Leu Trp Arg Ile
 88 225             230             235             240
 90 aag agg ttc ttc cac gtc ggg tca gag gcc ctc cta gcg cag agc atc    768
 91 Lys Arg Phe Phe His Val Gly Ser Glu Ala Leu Leu Ala Gln Ser Ile
 92             245             250             255
 94 aag ctc gtg gac gag ttc acc tac agc gtg atc cgc cgg agg aag gcc    816
 95 Lys Leu Val Asp Glu Phe Thr Tyr Ser Val Ile Arg Arg Arg Lys Ala
 96             260             265             270
 98 gag atc gtc gag gtc cgg gcc agc ggc aaa cag gag aag atg aag cac    864
 99 Glu Ile Val Glu Val Arg Ala Ser Gly Lys Gln Glu Lys Met Lys His
100             275             280             285
102 gac atc ctg tca cgg ttc atc gag ctg ggc gag gcc ggc gac gac ggc    912
103 Asp Ile Leu Ser Arg Phe Ile Glu Leu Gly Glu Ala Gly Asp Asp Gly
104             290             295             300
106 ggc ggc ttc ggg gac gat aag agc ctc cgg gac gtg gtg ctc aac ttc    960
107 Gly Gly Phe Gly Asp Asp Lys Ser Leu Arg Asp Val Val Leu Asn Phe
108 305             310             315             320
110 gtg atc gcc ggg cgg gac acg acg gcg acg acg ctg tcg tgg ttc acg   1008
111 Val Ile Ala Gly Arg Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Thr
112             325             330             335
114 cac atg gcc atg tcc cac ccg gac gtg gcc gag aag ctg cgc cgc gag   1056
115 His Met Ala Met Ser His Pro Asp Val Ala Glu Lys Leu Arg Arg Glu
116             340             345             350
118 ctg tgc gcg ttc gag gcg gag cgc gcg cgc gag gag ggc gtc acg ctc   1104
119 Leu Cys Ala Phe Glu Ala Glu Arg Ala Arg Glu Glu Gly Val Thr Leu
120             355             360             365
122 gtg ctc tgc ggc ggc gct gac gcc gac gac aag gcg ttc gcc gcc cgc   1152
123 Val Leu Cys Gly Gly Ala Asp Ala Asp Asp Lys Ala Phe Ala Ala Arg
124             370             375             380
126 gtg gcg cag ttc gcg ggc ctc ctc acc tac gac agc ctc ggc aag ctg   1200
127 Val Ala Gln Phe Ala Gly Leu Leu Thr Tyr Asp Ser Leu Gly Lys Leu
128 385             390             395             400
130 gtc tac ctc cac gcc tgc gtc acc gag acg ctc cgc ctg tac ccc gcc   1248
131 Val Tyr Leu His Ala Cys Val Thr Glu Thr Leu Arg Leu Tyr Pro Ala
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RAW SEQUENCE LISTING   DATE: 01/15/2002
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Input Set : A:\1148.app
Output Set: N:\CRF3\01152002\J021657.raw

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132              405              410              415
134 gtc cct cag gac ccc aag ggg atc ctg gag gac gac gtg ctg ccg gac    1296
135 Val Pro Gln Asp Pro Lys Gly Ile Leu Glu Asp Asp Val Leu Pro Asp
136              420              425              430
138 ggg acg aag gtg agg gcc ggc ggg atg gtg acg tac gtg ccc tac tcg    1344
139 Gly Thr Lys Val Arg Ala Gly Gly Met Val Thr Tyr Val Pro Tyr Ser
140              435              440              445
142 atg ggg cgg atg gag tac aac tgg ggc ccc gac gcg gcg agc ttc cgg    1392
143 Met Gly Arg Met Glu Tyr Asn Trp Gly Pro Asp Ala Ala Ser Phe Arg
144      450              455              460
146 ccg gag cgg tgg atc aac gag gat ggc gcg ttc cgc aac gcg tcg ccg    1440
147 Pro Glu Arg Trp Ile Asn Glu Asp Gly Ala Phe Arg Asn Ala Ser Pro
148 465              470              475              480
150 ttc aag ttc acg gcg ttc cag gcg ggg ccg agg atc tgc ctg ggc aag    1488
151 Phe Lys Phe Thr Ala Phe Gln Ala Gly Pro Arg Ile Cys Leu Gly Lys
152              485              490              495
154 gac tcg gcg tac ctg cag atg aag atg gcg ctg gcc atc ctc ttc cgc    1536
155 Asp Ser Ala Tyr Leu Gln Met Lys Met Ala Leu Ala Ile Leu Phe Arg
156              500              505              510
158 ttc tac agc ttc cgg ctg ctg gag ggg cac ccg gtg cag tac cgc atg    1584
159 Phe Tyr Ser Phe Arg Leu Leu Glu Gly His Pro Val Gln Tyr Arg Met
160      515              520              525
162 atg acc atc ctc tcc atg gcg cac ggc ctc aag gtc cgc gtc tct agg    1632
163 Met Thr Ile Leu Ser Met Ala His Gly Leu Lys Val Arg Val Ser Arg
164      530              535              540
166 gcc gtc tga tgt cat ggc gat ttg gat atg gat atc gtc ccg ctt aat    1680
167 Ala Val     Cys His Gly Asp Leu Asp Met Asp Ile Val Pro Leu Asn
168 545              550              555
170 cca cga caa ata acg ctc gtg tta caa att tgc atg cat gca tgt aag    1728
171 Pro Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys
172 560              565              570              575
174 gga aag cga tgg gtt tca ttg gtg gct tgg ctt aag cct taaaaactcc    1777
175 Gly Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro
176              580              585
178 gtcgggtctt gcgaaccacc acatcactag tgttttgtac tctactcctc agtggaagtg    1837
180 tagtgacagc atacaagttc atcatatata ttatcctctt tcttaaaaaa aaaaaaaaaa    1897
182 aaactcgag    1906
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 588
187 <212> TYPE: PRT
188 <213> ORGANISM: Zea mays
190 <400> SEQUENCE: 2
191 Glu Phe Gly Thr Arg Glu Ala His Leu Thr Pro Ala Thr Pro Ser Pro
192   1              5              10              15
194 Phe Phe Pro Leu Ala Gly Pro His Lys Tyr Ile Ala Leu Leu Leu Val
195              20              25              30
197 Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys
198      35              40              45
200 Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg
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Input Set : A:\1148.app
Output Set: N:\CRF3\01152002\J021657.raw

```
201      50                  55                    60
203 Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His
204   65            70                75                80
206 Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala
207              85                90                95
209 Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr
210             100               105               110
212 Pro Lys Gly Ile Val Tyr Arg Ser Tyr Met Asp Val Leu Leu Gly Asp
213          115               120               125
215 Gly Ile Phe Asn Ala Asp Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr
216    130               135               140
218 Ala Ser Phe Glu Phe Ala Ser Lys Asn Leu Arg Asp Phe Ser Ala Ile
219 145               150               155               160
221 Val Phe Arg Glu Tyr Ser Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala
222             165               170               175
224 Ser Lys Ala Gly Lys Val Val Asp Met Gln Glu Leu Tyr Met Arg Met
225          180               185               190
227 Thr Leu Asp Ser Ile Cys Lys Val Gly Phe Gly Val Glu Ile Gly Thr
228          195               200               205
230 Leu Ser Pro Asp Leu Pro Glu Asn Ser Phe Ala Gln Ala Phe Asp Ala
231    210               215               220
233 Ala Asn Ile Ile Ile Thr Leu Arg Phe Ile Asp Pro Leu Trp Arg Ile
234 225               230               235               240
236 Lys Arg Phe Phe His Val Gly Ser Glu Ala Leu Leu Ala Gln Ser Ile
237             245               250               255
239 Lys Leu Val Asp Glu Phe Thr Tyr Ser Val Ile Arg Arg Arg Lys Ala
240          260               265               270
242 Glu Ile Val Glu Val Arg Ala Ser Gly Lys Gln Glu Lys Met Lys His
243          275               280               285
245 Asp Ile Leu Ser Arg Phe Ile Glu Leu Gly Glu Ala Gly Asp Asp Gly
246    290               295               300
248 Gly Gly Phe Gly Asp Asp Lys Ser Leu Arg Asp Val Val Leu Asn Phe
249 305               310               315               320
251 Val Ile Ala Gly Arg Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Thr
252          325               330               335
254 His Met Ala Met Ser His Pro Asp Val Ala Glu Lys Leu Arg Arg Glu
255          340               345               350
257 Leu Cys Ala Phe Glu Ala Glu Arg Ala Arg Glu Glu Gly Val Thr Leu
258    355               360               365
260 Val Leu Cys Gly Gly Ala Asp Ala Asp Asp Lys Ala Phe Ala Ala Arg
261    370               375               380
263 Val Ala Gln Phe Ala Gly Leu Leu Thr Tyr Asp Ser Leu Gly Lys Leu
264 385               390               395               400
266 Val Tyr Leu His Ala Cys Val Thr Glu Thr Leu Arg Leu Tyr Pro Ala
267             405               410               415
269 Val Pro Gln Asp Pro Lys Gly Ile Leu Glu Asp Asp Val Leu Pro Asp
270          420               425               430
272 Gly Thr Lys Val Arg Ala Gly Gly Met Val Thr Tyr Val Pro Tyr Ser
273          435               440               445
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PATENT APPLICATION: US/10/021,657   TIME: 19:02:43

Input Set : A:\1148.app
Output Set: N:\CRF3\01152002\J021657.raw

```
275 Met Gly Arg Met Glu Tyr Asn Trp Gly Pro Asp Ala Ala Ser Phe Arg
276   450               455               460
278 Pro Glu Arg Trp Ile Asn Glu Asp Gly Ala Phe Arg Asn Ala Ser Pro
279 465               470               475               480
281 Phe Lys Phe Thr Ala Phe Gln Ala Gly Pro Arg Ile Cys Leu Gly Lys
282               485               490               495
284 Asp Ser Ala Tyr Leu Gln Met Lys Met Ala Leu Ala Ile Leu Phe Arg
285               500               505               510
287 Phe Tyr Ser Phe Arg Leu Leu Glu Gly His Pro Val Gln Tyr Arg Met
288               515               520               525
290 Met Thr Ile Leu Ser Met Ala His Gly Leu Lys Val Arg Val Ser Arg
291       530               535               540
293 Ala Val Cys His Gly Asp Leu Asp Met Asp Ile Val Pro Leu Asn Pro
294 545               550               555               560
296 Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys Gly
297               565               570               575
299 Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro
300               580               585
303 <210> SEQ ID NO: 3
304 <211> LENGTH: 494
305 <212> TYPE: DNA
306 <213> ORGANISM: Sorghum sp.
308 <220> FEATURE:
309 <221> NAME/KEY: modified_base
310 <222> LOCATION: (1)..(494)
311 <223> OTHER INFORMATION: "n" bases may be a, t, c, g, other or unknown
313 <400> SEQUENCE: 3
314 ggaattcggc ttatgccgtt cacttcctac acctacatcg ctgacccggt gaatgtcgag 60
315 catgtcctca agactaactt caccaattac cccaaggggg acgtgtacag atcctacatg 120
316 gatgtgctcc tcggtgacgg catattcaac gctgacggcg agctgtggag gaagcagagg 180
317 aagacggcga gtttcgagtt cgcctccaag aacctgaggg atttcagtgc caatgttttc 240
318 agagagtact ccctgaagct gtcgggcata ctgagtcagg catccaaggc aggcaaagtt 300
319 gttgacatgc aggaacttta catgaggatg acactggact cgatctgcaa ngttgggttc 360
320 ggggtcnana tcggcacgct gtcnccggat ctccccgaga acagcttcnc ccaagcgttc 420
321 gatgccgcta acatcatcgt cacnctgcgg ttcatccacc cnctgtggcg catccagaag 480
322 ttcttcccn gtca 494
325 <210> SEQ ID NO: 4
326 <211> LENGTH: 158
327 <212> TYPE: PRT
328 <213> ORGANISM: Sorghum sp.
330 <220> FEATURE:
331 <221> NAME/KEY: MOD_RES
332 <222> LOCATION: (1)..(158)
333 <223> OTHER INFORMATION: "Xaa" may be any, other or unknown amino acid
335 <400> SEQUENCE: 4
336 Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala Asp Pro Val Asn Val Glu
337   1               5               10               15
339 His Val Leu Lys Thr Asn Phe Thr Asn Tyr Pro Lys Gly Asp Val Tyr
340               20               25               30
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W--> (lines 319–322)

VERIFICATION SUMMARY   DATE: 01/15/2002
PATENT APPLICATION: **US/10/021,657**   TIME: 19:02:44

Input Set : **A:\1148.app**
Output Set: **N:\CRF3\01152002\J021657.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4